C2 consists of residues 1-120, the C_H1 domain 121-218, the modified hinge 219-238, and the Fos leucine zipper 239-279.

Please replace the paragraph beginning on page 22, line 29, with the following replacement paragraph:

In a further approach, bispecific antibodies are formed by linking component antibodies to leucine zipper peptides. *See generally* copending application 07/801,798, filed November 29, 1991; Kostelny et al., *J. Immunol.* 148, 1547-1553 (1992) (incorporated by reference in their entirety for all purposes). Leucine zippers have the general structural formula (Leucine-X_1-X_2-X_3-X_4-X_5-X_6)$_n$ (SEQ ID NO:14), where X may be any of the conventional 20 amino acids (*Proteins, Structures and Molecular Principles*, (1984) Creighton (ed.), W.H. Freeman and Company, New York), but are most likely to be amino acids with high α-helix forming potential, for example, alanine, valine, aspartic acid, glutamic acid, and lysine (Richardson and Richardson, *Science* 240, 1648 (1988)), and n may be 3 or greater, although typically n is 4 or 5. The leucine zipper occurs in a variety of eukaryotic DNA-binding proteins, such as GCN4, C/EBP, c-fos gene product (Fos), c-jun gene product (Jun), and c-myc gene product. In these proteins, the leucine zipper creates a dimerization interface wherein proteins containing leucine zippers may form stable homodimers and/or heterodimers.

C3

Please insert the accompanying paper copy of the sequence listing, page numbers 1-20, at the end of the application.

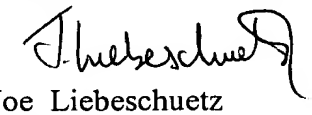
REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§ 1.821-1.825. The information contained in the computer readable disk of Application No. 08/832,985 was prepared through use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the specification by the amendment. The attached page is captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



Joe Liebeschuetz
Reg. No. 37,505

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (650) 326-2400
Fax: (650) 326-2422
JOL:adm
PA 3175044 v1

VERSION WITH MARKINGS TO SHOW CHANGES MADE

The paragraph beginning on page 6, line 12, has been amended as follows:

Figure 4. Amino acid sequences of the light chain (A) (SEQ ID NOS:1-2) and the heavy chain (B) (SEQ ID NOS:3-4) variable regions of the humanized 1D10 antibody (upper lines) and mouse 1D10 antibody (lower lines), not including the signal sequences. The three CDRs in each chain are underlined. Residues in the human framework that have been replaced with mouse amino acids or consensus human amino acids are doubly underlined. Amino acid sequences of the complete light chain and the heavy chain of the humanized 1D10 are [showed] shown in (C)(SEQ ID NO:5) and (E) (SEQ ID NO:7), respectively. The V_L domain consists of residues 1-107, and the C_K 108-214. The V_H domain consists of residues 1-116, the C_H1 117-214, the hinge 215-229, the C_H2 230-339, and the C_H3 domain 340-446. Amino acid sequence of the Fd-Jun in the humanized F(ab'-zipper)$_2$ of 1D10 is shown in (D) (SEQ ID NO:6). The V_H domain consists of residues 1-116, the C_H1 domain 117-214, the modified hinge 215-234, and the Fos leucine zipper 235-273.

The paragraph beginning on page 6, line 28, has been amended as follows:

Figure 5. Amino acid sequence of the light chain (A) (SEQ ID NOS:8-9) and the heavy chain (B) (SEQ ID NOS:10-11) variable regions of the humanized M291 antibody (upper lines) and the mouse M291 antibody (lower lines), not including the signal sequences. The three CDRs in each chain are underlined. Residues in the human framework that have been replaced with mouse amino acids or consensus human amino acids are doubly underlined. Amino acid sequences of the complete light chain of the humanized M291 are [showed] shown in (C) (SEQ ID NO:12). The V_L domain consists of residues 1-106, and the human C_K domain 107-213. Amino acid sequence of the Fd-Fos in the humanized F(ab'zipper)2 of M291 is shown in D (SEQ ID NO:13). The V_H domain consists of residues 1-120, the C_H1 domain 121-218, the modified hinge 219-238, and the Fos leucine zipper 239-279.

The paragraph beginning on page 22, line 29, has been amended as follows:

In a further approach, bispecific antibodies are formed by linking component antibodies to leucine zipper peptides. *See generally* copending application [11823-003200 (]07/801,798, filed November 29, 1991; Kostelny et al., *J. Immunol.* 148, 1547-1553 (1992) (incorporated by reference in their entirety for all purposes). Leucine zippers have the general structural formula (Leucine-X_1-X_2-X_3-X_4-X_5-X_6)$_n$ (SEQ ID NO:14), where X may be any of the conventional 20 amino acids (*Proteins, Structures and Molecular Principles*, (1984) Creighton (ed.), W.H. Freeman and Company, New York), but are most likely to be amino acids with high α-helix forming potential, for example, alanine, valine, aspartic acid, glutamic acid, and lysine (Richardson and Richardson, *Science* 240, 1648 (1988)), and n may be 3 or greater, although typically n is 4 or 5. The leucine zipper occurs in a variety of eukaryotic DNA-binding proteins, such as GCN4, C/EBP, c-fos gene product (Fos), c-jun gene product (Jun), and c-myc gene product. In these proteins, the leucine zipper creates a dimerization interface wherein proteins containing leucine zippers may form stable homodimers and/or heterodimers.